

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/960,738A

DATE: 02/26/2002 TIME: 13:59:55

Input Set : A:\032301.218.ST25.txt

Output Set: N:\CRF3\02262002\I960738A.raw

```
3 :110> APPLICANT: BATHE, Brigitte, et al.
      5 :120 - TITLE OF INVENTION: NUCLEOTIDE SEQUENCES WHICH CODE FOR THE PPKK GENE
      7 -: 130. FILE REFERENCE: 032301 WD 218
C--> 9 <140> CURRENT APPLICATION NUMBER: US/09/960,738A
C--> 9 <141> CURRENT FILING DATE: 2001-09-24
      9 -1160 NUMBER OF SEQ ID NOS: 2
     11 · 170 · SOFTWARE: PatentIn version 3.1
     13 - 1210 - SEQ ID NO: 1
     14 -: 211: LENGTH: 1239
     15 -: 212: TYPE: DNA
     16 <213: ORGANISM: Corynebacterium glutamicum
     18 -:220> FEATURE:
     19 <221> NAME/KEY: CDS
     20 (222) LOCATION: (237)..(1022)
     21 <223> OTHER INFORMATION:
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    25 ggccgaagtt cctgcaacct attggcgata aaatcttcag ccaaagtatc tactatcgtc
                                                                                60
    27 accggatega etgtegaaet tttggtgttg gtgtagtece acaaattggt gagtteagea
                                                                              120
    29 cgcttatccc tgatacgtac agcggtaagc gtggcagttt ccgcggcgat ggcacgcaac
                                                                              180
    31 tcattaaacg attgttgttc cataagacca tcatcgttgt ttttttagaa aattgc ctg
                                                                              239
    32
    33
    35 cca aaa gcc gaa gta att tgt aca ctt ggg cgc atg act gag act gga
                                                                              287
    36 Pro Lys Ala Glu Val Ile Cys Thr Leu Gly Arg Met Thr Glu Thr Gly
                                        10
    39 ttt gga att gat atc ggt ggc tcc ggc atc aaa ggc gcc cgc gtt aac
                                                                              335
    40 Phe Gly Ile Asp Ile Gly Gly Ser Gly Ile Lys Gly Ala Arg Val Asn
    41
               20
    43 ctt aag acc ggt gag ttt att gat gaa cgc ata aaa atc gcc acc cct
                                                                              383
    44 Leu Lys Thr Gly Glu Phe Ile Asp Glu Arg Ile Lys Ile Ala Thr Pro
    47 aag cca gca acc cca gag gct gtc gcc gaa gta gtc gca gag att att
                                                                              431
    48 Lys Pro Ala Thr Pro Glu Ala Val Ala Glu Val Val Ala Glu Ile Ile
    49 50
                            55
    51 tct caa gcc gaa tgg gag ggt ccg gtc gga att acc ctg ccg tcg gtc
                                                                              479
    52 Ser Gln Ala Glu Trp Glu Gly Pro Val Gly Ile Thr Leu Pro Ser Val
                       70
    55 gtt cgc ggg cag atc gcg cta tcc gca gcc aac att gac aag tcc tgg
                                                                              527
    56 Val Arg Gly Gln Ile Ala Leu Ser Ala Ala Asn Ile Asp Lys Ser Trp
                   85
                                        90
    59 atc ggc acc gat gtg cac gaa ctt ttt gac cgc cac cta aat ggc cga
                                                                              575
    60 Ile Gly Thr Asp Val His Glu Leu Phe Asp Arg His Leu Asn Gly Arg
    61
               100
```

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63 gag atc acc gtt c	to aat gad gda	gac gee gee gge ate gee gaa gea	623							
		Asp Ala Ala Gly Ile Ala Glu Ala								
65 115	120	125								
67 acc ttt ggc aac c	ct gcc gca cgc	gaa ggc gca gtc atc ctg ctg acc	671							
68 Thr Phe Gly Asn P.	ro Ala Ala Arg	Glu Gly Ala Val Ile Leu Leu Thr								
69 130	135	140 145								
71 ott ggt aca ggt a	tt gga tcc gca	tto ctt gtg gat ggc caa ctg ttc	719							
72 Leu Gly Thr Gly I	le Gly Ser Ala	Phe Leu Val Asp Gly Gln Leu Phe								
· -	50	155 160								
		atc gtt gac ggc gag gaa gca gaa	767							
	eu Gly His Met	Ile Val Asp Gly Glu Glu Ala Glu								
77 165		170 175	015							
		gaa aac gaa gat ctg tca tgg aag	815							
		Glu Asn Glu Asp Leu Ser Trp Lys								
81 180	185	190	863							
		gtg ctg agc gaa tac gag aaa ctt Val Leu Ser Glu Tyr Glu Lys Leu	003							
85 195	200	205								
		ggt ggc gga att tcc aga aag cac	911							
		Gly Gly Gly Ile Ser Arg Lys His	7++							
89 210	215	220 225								
		cta gac act gac att gtc cca gct	959							
		Leu Asp Thr Asp Ile Val Pro Ala								
• •	30	235 240								
95 gag ctg cgc aat c	ga gcc gga atc	gta gga gct gcc atg gca gta aac	1007							
		Val Gly Ala Ala Met Ala Val Asn								
97 245		250 255								
99 caa cac ctc acc c	ca taagttatcg a	aaaggtgatt tttgcccagg gccttgattc	1062							
100 Gln His Leu Thr	Pro									
101 260			1100							
		gc ccctttgtga catcggcgta gttgttcaac	1122							
		gt taaccatgag attgattcac ccctttaagc	1182 1239							
		tt cggcatttaa aaaagccgag agcaaat	1233							
110 <210> SEQ ID NO:										
111 <211> LENGTH: 262 112 <212> TYPE: PRT										
113 <213> ORGANISM:	Corvnebacterium	m qlutamicum								
115 (400) SEQUENCE:	-	m gracamroum								
		s Thr Leu Gly Arg Met Thr Glu Thr								
	5	10 15								
	Asp Ile Gly Gly	y Ser Gly Ile Lys Gly Ala Arg Val								
122 20		25 30								
125 Asn Leu Lys Thr	Gly Glu Phe Ile	e Asp Glu Arg Ile Lys Ile Ala Thr								
126 35	40	45								
129 Pro Lys Pro Ala	Thr Pro Glu Ala	a Val Ala Glu Val Val Ala Glu Ile								
130 50	55	60								
		y Pro Val Gly Ile Thr Leu Pro Ser								
134 65	70	75 80								
137 Val Val Arg Gly	Gin lle Ala Lei	u Ser Ala Ala Asn Ile Asp Lys Ser								

RAW SEQUENCE LISTING

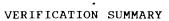
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138					85					90					95	
141	Trp	Ile	Gly	Thr	Asp	Val	His	Glu	Leu	Phe	Asp	Arg	His	Leu	Asn	Gly
14.2				100					105					110		
145	Arg	Glu	Ile	Thr	Val	Leu	Asn	Asp	Ala	Asp	Ala	Ala	Gly	Ile	Ala	Glu
146			115					120					125			
149	Ala	Thr	Phe	Gly	Asn	Pro	Ala	Ala	Arg	Glu	Gly	Ala	Val	Ile	Leu	Leu
150		130					135					140				
153	Thr	Leu	Gly	Thr	Gly	Ile	Gly	Ser	Ala	Phe	Leu	Val	Asp	Gly	Gln	Leu
	145					150					155					160
157	Phe	Pro	Asn	Thr	Glu	Leu	Gly	His	Met	Ile	Val	Asp	Gly	Glu	Glu	Ala
158					165					170					175	
161	Glu	His	Leu	Ala	Ala	Ala	Ser	Val	Lys	Glu	Asn	Glu	Asp	Leu	Ser	Trp
162				180					185					190		
165	Lys	Lys	Trp	Ala	Lys	His	Leu	Asn	Lys	Val	Leu	Ser	Glu	Tyr	Glu	Lys
166			195					200					205			
169	Leu	Phe	Ser	Pro	Ser	Val	Phe	Ile	Ile	Gly	Gly	Gly	Ile	Ser	Arg	Lys
170		210					215					220				
173	His	Glu	Lys	Trp	Leu	Pro	Leu	Met	Glu	Leu	Asp	Thr	Asp	Ile	Val	
	225					230					235					240
177	Ala	Glu	Leu	Arg	Asn	Arg	Ala	Gly	Ile	Val	Gly	Ala	Ala	Met		Val
178					245					250					255	
181	Asn	Gln	His	Leu	Thr	Pro										
182				260												



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L:9 M:270 C: Current Application Number differs, Replaced Current Application No

L:9 M:271 C: Current Filing Date differs, Replaced Current Filing Date